



0300

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/819,144
Source: OIPÉ
Date Processed by STIC: 6/13/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

01PE

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/819,144

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

Does Not Comply
Corrected No Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/819,144

DATE: 06/13/2003

TIME: 08:30:03

Error on p. 2

Input Set : A:\21486-021DIV.txt

Output Set: N:\CRF4\06132003\I819144.raw

4 <110> APPLICANT: Terek, Richard M.
6 <120> TITLE OF INVENTION: CHONDROSARCOMA ASSOCIATED GENES
8 <130> FILE REFERENCE: 21486-021DIV
10 <140> CURRENT APPLICATION NUMBER: US 09/819,144
C--> 11 <141> CURRENT FILING DATE: 2003-06-06
13 <160> NUMBER OF SEQ ID NOS: 8
15 <170> SOFTWARE: FastSEQ for Windows Version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 164
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)...(156)
26 <400> SEQUENCE: 1
27 atg gct gcg ggt ccc agg cca gga gct ccc tgc agg gcg ggg gct ccc 48
28 Met Ala Ala Gly Pro Arg Pro Gly Ala Pro Cys Arg Ala Gly Ala Pro
29 1 5 10 15
31 acg atc gta ttg acc tct gga aga aga cag aca ctt tcc cac ggg agc 96
32 Thr Ile Val Leu Thr Ser Gly Arg Arg Gln Thr Leu Ser His Gly Ser
33 20 25 30
35 tcc tct cca gcc aga gct aca ctt ggc aaa cct ttg gtc cta aat gat 144
36 Ser Ser Pro Ala Arg Ala Thr Leu Gly Lys Pro Leu Val Leu Asn Asp
37 35 40 45
39 tat tca ctg aat tgaagaaa 164
40 Tyr Ser Leu Asn
41 50
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 52
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 2
50 Met Ala Ala Gly Pro Arg Pro Gly Ala Pro Cys Arg Ala Gly Ala Pro
51 1 5 10 15
52 Thr Ile Val Leu Thr Ser Gly Arg Arg Gln Thr Leu Ser His Gly Ser
53 20 25 30
54 Ser Ser Pro Ala Arg Ala Thr Leu Gly Lys Pro Leu Val Leu Asn Asp
55 35 40 45
56 Tyr Ser Leu Asn
57 50
59 <210> SEQ ID NO: 3
60 <211> LENGTH: 884
61 <212> TYPE: DNA

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/819,144

DATE: 06/13/2003

TIME: 08:30:03

Input Set : A:\21486-021DIV.txt

Output Set: N:\CRF4\06132003\I819144.raw

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62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 3
65 acttccctgg gttcacagca ggggtggaac tggattcttc ctggatgggg atccagatgg      60
66 aggtggagct gcaccccttg tagagaatgg ctgcgggtcc caggccagga gctccctgca      120
67 gggcgggggc tcccacgatc gtattgacct ctggaagaag acagacactt tcccacggga      180
68 gctcctctcc agccagagct acacttggca aacctttggt cctaaatgat tattcactga      240
69 attgaagaaa tacggtttac atatcttcca agtatatatg tagggttgat ttgggaagca      300
70 gaacacagca gcccaaattt gcttgtaatg tctgcgacta cagcctgctg gcctgccttc      360
71 actgtcttgg gggaagctcg gggagaccag gtggactgga gtagactgtg cagagacact      420
72 ggtctggtga agatgtccag gaaaccacga gcctccagcc cattttccaa caaccacca      480
73 tcaacaccaa agaggttccc aagacaaccc agaagggaaa agggaccctg caaggaagtt      540
74 ccaggaacaa aaggctctcc ctaaaagacc accgcttcaa aaaaacctga ggaatggagt      600
75 gggccaacac tatccagcca ctctgaccag ccgaacgagg aactcaatca aaatgcgcca      660
76 tagcaggacc acaagggcaa ggagaccacc gccttctcca gtgcttcctt gggcagccag      720
77 taattcccag gcaaggccag agacttcaag tctatctgaa aagtctccag aagtctaacc      780
78 ccagataaat agccaacagg gtgtagagta cgttttacac ccaaagggtg atgccccatg      840
79 gtgatggaaa taaaatgaac atgttgtaaa atgaaaaaaaa aaaa      884

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81 <210> SEQ ID NO: 4

82 <211> LENGTH: 14

83 <212> TYPE: DNA

84 <213> ORGANISM: Artificial Sequence

86 <220> FEATURE:

87 <223> OTHER INFORMATION: Artificial sequence

89 <220> FEATURE:

90 <221> NAME/KEY: misc_feature

91 <222> LOCATION: (1)...(14)

92 <223> OTHER INFORMATION: n = A,T,C or G

94 <400> SEQUENCE: 4

W--> 95 tttttttttt ttvn

14

97 <210> SEQ ID NO: 5

98 <211> LENGTH: 1946

99 <212> TYPE: DNA

100 <213> ORGANISM: Homo sapiens

102 <220> FEATURE:

103 <221> NAME/KEY: misc_feature

104 <222> LOCATION: (1)...(1946)

105 <223> OTHER INFORMATION: n = A,T,C or G

107 <400> SEQUENCE: 5

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108 cacgcaaagc agtgtgggtt gattctgagg tgcactgtgg gaaagagctt gtcgctgcgg      60
109 tggtgctggt ggagactcga ttgttggtga cagcgaaaga acgataacaa aatgccggag      120
110 cgagatagtg agccgttctc caaccctttg gccccgatg gccacgatgt ggatgacct      180
W--> 111 cactccttcc accaatcaaa actcaccaat gaagacttca ggaaantnnt catgaccccc      240
112 agggntgcac ntacntntgc accacnttnt aantnnntc accatgagat gccaaggag      300
113 tacaatgagg atgaagaccc agctgcacga aggaggaaaa agaaaagtta ttatgccaa      360
114 ctacgccaac aagaaattga gagagagaga gagctagcag agaagtaccg ggatcgtgcc      420
115 aaggaacgga gagatggagt gaacaaagat tatgaagaaa ccgagcttat cagcaccaca      480
116 gctaactata gggctgttgg cccactgct gaggcggaca aatcagctrc agnnragaga      540
117 agacanwnda hcnaggagtc caaattcttg ggtggtgaca tggaacacac ccatttggtg      600
118 aaaggcttgg attttgntnt gcttchnaan gtncgagctg agattgncms cmnanaraaa      660

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— must explain genetic source —
See error summary sheet item 11

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/819,144

DATE: 06/13/2003

TIME: 08:30:03

Input Set : A:\21486-021DIV.txt

Output Set: N:\CRF4\06132003\I819144.raw

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119 nargaarang nnctgatggn aaancccmg aaagaaacca agaaagatga ggatcctgaa 720
120 aataaaattg aattttaaac acgtctgggc cgcaatgttt accgaatgct ttttaagagc 780
121 aaagcatatg agcggaatga gttgttcctg ccgggccgca tggcctatgt ggtagacctg 840
122 gatgatgagt atgctgacac agatatcccc accactctta tcccgagca aggctgattg 900
123 cccaccatg gaggccaga ccacactgac cacaaatgac attgtcatta gcaagctgac 960
124 ccagatcctt tcatacctga ggcagggaac ccgtaacaag aagcttaaga agaaggataa 1020
125 aggggaagccg gaagagaaga aacctcctga ggctgacatg aatatttttg aagacattgg 1080
126 ggattacgta ccctccacaa ccaagacacc tcgggacaag gagcgggaga gatatcggga 1140
127 acgggagcgt gatcgggaaa gagacagaga ccgtgaccga gagcgagagc gagaacgaga 1200
128 tcgggaacga gagcgagagc gggaccgaga gagagaagag gaaaagaaga gacacagcta 1260
129 ctttgagaag ccaaaagtag atgatgagcc catggacgtt gacaaaggac ctgggtctac 1320
130 caaggagttg atcaagtcca tcaatgaaaa gtttgctggg tctgctggct gggaaggcac 1380
131 agaatcgctg aagaagccag aagacaaaaa gcagctggga gatttctttg gcatgtccaa 1440
132 cagttatgca gagtgctacc cagccacgat ggatgacatg gctgtggata gtgatgagga 1500
133 ggtggattat agcaaaatgg accagggtaa caagaagggg cccttaggcc gttgggactt 1560
134 tgatacccag gaagaataca gcgagtatat gaacaacaaa gaagctttgc ccaaggctgc 1620
135 attccagtat ggtatcaaaa tgtctgaagg gcggaaaacc aggcgcttca aggaaaccaa 1680
136 tgacaaagca gagcttgatc gccagtggaa gaagattagt gcaatcattg angaagagga 1740
137 agaagatgga agctgatggg gttgaagtca aaagacaaa atactaatca ctagttacaa 1800
138 ccagagatgc tccacaagga tatgctcccc actgttttct ttctacaatt tccaaagggt 1860
139 gcaagatgtt tttttgtgat gaatataaaa ttttattgtg taattacttg gttccattaa 1920
140 aattggttaa cttgctaaaa aaaaaa 1946
142 <210> SEQ ID NO: 6
143 <211> LENGTH: 915
144 <212> TYPE: DNA
145 <213> ORGANISM: Homo sapiens
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (1)...(912)
151 <220> FEATURE:
152 <221> NAME/KEY: misc_feature
153 <222> LOCATION: (1)...(915)
154 <223> OTHER INFORMATION: n = A,T,C or G
156 <400> SEQUENCE: 6
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158 Met Met Ser Met Leu Thr Gln Ile Ser Pro Pro Leu Leu Ser Arg Ser
159 1 5 10 15
161 aag gct gat tgc ccc acc atg gag gcc cag acc aca ctg acc aca aat 96
162 Lys Ala Asp Cys Pro Thr Met Glu Ala Gln Thr Thr Leu Thr Thr Asn
163 20 25 30
165 gac att gtc att agc aag ctg acc cag atc ctt tca tac ctg agg cag 144
166 Asp Ile Val Ile Ser Lys Leu Thr Gln Ile Leu Ser Tyr Leu Arg Gln
167 35 40 45
169 gga acc cgt aac aag aag ctt aag aag aag gat aaa ggg aag ccg gaa 192
170 Gly Thr Arg Asn Lys Lys Leu Lys Lys Lys Asp Lys Gly Lys Pro Glu
171 50 55 60
173 gag aag aaa cct cct gag gct gac atg aat att ttt gaa gac att ggg 240
174 Glu Lys Lys Pro Pro Glu Ala Asp Met Asn Ile Phe Glu Asp Ile Gly
175 65 70 75 80

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/819,144

DATE: 06/13/2003

TIME: 08:30:03

Input Set : A:\21486-021DIV.txt

Output Set: N:\CRF4\06132003\I819144.raw

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177  gat tac gta ccc tcc aca acc aag aca cct cgg gac aag gag cgg gag      288
178  Asp Tyr Val Pro Ser Thr Thr Lys Thr Pro Arg Asp Lys Glu Arg Glu
179              85                      90                      95
181  aga tat cgg gaa cgg gag cgt gat cgg gaa aga gac aga gac cgt gac      336
182  Arg Tyr Arg Glu Arg Glu Arg Asp Arg Glu Arg Asp Arg Asp Arg Asp
183              100                      105                      110
185  cga gag cga gag cga gaa cga gat cgg gaa cga gag cga gag cgg gac      384
186  Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg Glu Arg Glu Arg Asp
187              115                      120                      125
189  cga gag aga gaa gag gaa aag aag aga cac agc tac ttt gag aag cca      432
190  Arg Glu Arg Glu Glu Glu Lys Lys Arg His Ser Tyr Phe Glu Lys Pro
191              130                      135                      140
193  aaa gta gat gat gag ccc atg gac gtt gac aaa gga cct ggg tct acc      480
194  Lys Val Asp Asp Glu Pro Met Asp Val Asp Lys Gly Pro Gly Ser Thr
195  145                      150                      155                      160
197  aag gag ttg atc aag tcc atc aat gaa aag ttt gct ggg tct gct ggc      528
198  Lys Glu Leu Ile Lys Ser Ile Asn Glu Lys Phe Ala Gly Ser Ala Gly
199              165                      170                      175
201  tgg gaa ggc aca gaa tcg ctg aag aag cca gaa gac aaa aag cag ctg      576
202  Trp Glu Gly Thr Glu Ser Leu Lys Lys Pro Glu Asp Lys Lys Gln Leu
203              180                      185                      190
205  gga gat ttc ttt ggc atg tcc aac agt tat gca gag tgc tac cca gcc      624
206  Gly Asp Phe Phe Gly Met Ser Asn Ser Tyr Ala Glu Cys Tyr Pro Ala
207              195                      200                      205
209  acg atg gat gac atg gct gtg gat agt gat gag gag gtg gat tat agc      672
210  Thr Met Asp Asp Met Ala Val Asp Ser Asp Glu Glu Val Asp Tyr Ser
211              210                      215                      220
213  aaa atg gac cag ggt aac aag aag ggg ccc tta ggc cgt tgg gac ttt      720
214  Lys Met Asp Gln Gly Asn Lys Lys Gly Pro Leu Gly Arg Trp Asp Phe
215  225                      230                      235                      240
217  gat acc cag gaa gaa tac agc gag tat atg aac aac aaa gaa gct ttg      768
218  Asp Thr Gln Glu Glu Tyr Ser Glu Tyr Met Asn Asn Lys Glu Ala Leu
219              245                      250                      255
221  ccc aag gct gca ttc cag tat ggt atc aaa atg tct gaa ggg cgg aaa      816
222  Pro Lys Ala Ala Phe Gln Tyr Gly Ile Lys Met Ser Glu Gly Arg Lys
223              260                      265                      270
225  acc agg cgc ttc aag gaa acc aat gac aaa gca gag ctt gat cgc cag      864
226  Thr Arg Arg Phe Lys Glu Thr Asn Asp Lys Ala Glu Leu Asp Arg Gln
227              275                      280                      285
W--> 229  tgg aag aag att agt gca atc att gan gaa gag gaa gaa gat gga agc      912
230  Trp Lys Lys Ile Ser Ala Ile Ile Xaa Glu Glu Glu Glu Asp Gly Ser
231              290                      295                      300
233  tga      915
235 <210> SEQ ID NO: 7
236 <211> LENGTH: 304
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <220> FEATURE:
241 <221> NAME/KEY: VARIANT

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/819,144

DATE: 06/13/2003

TIME: 08:30:03

Input Set : A:\21486-021DIV.txt

Output Set: N:\CRF4\06132003\I819144.raw

242 <222> LOCATION: (1)...(304)

243 <223> OTHER INFORMATION: Xaa = Any Amino Acid

245 <400> SEQUENCE: 7

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246 Met Met Ser Met Leu Thr Gln Ile Ser Pro Pro Leu Leu Ser Arg Ser
247   1           5           10           15
248 Lys Ala Asp Cys Pro Thr Met Glu Ala Gln Thr Thr Leu Thr Thr Asn
249           20           25           30
250 Asp Ile Val Ile Ser Lys Leu Thr Gln Ile Leu Ser Tyr Leu Arg Gln
251           35           40           45
252 Gly Thr Arg Asn Lys Lys Leu Lys Lys Lys Asp Lys Gly Lys Pro Glu
253   50           55           60
254 Glu Lys Lys Pro Pro Glu Ala Asp Met Asn Ile Phe Glu Asp Ile Gly
255   65           70           75           80
256 Asp Tyr Val Pro Ser Thr Thr Lys Thr Pro Arg Asp Lys Glu Arg Glu
257           85           90           95
258 Arg Tyr Arg Glu Arg Glu Arg Asp Arg Glu Arg Asp Arg Asp Arg Asp
259           100          105          110
260 Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg Glu Arg Glu Arg Asp
261           115          120          125
262 Arg Glu Arg Glu Glu Glu Lys Lys Arg His Ser Tyr Phe Glu Lys Pro
263           130          135          140
264 Lys Val Asp Asp Glu Pro Met Asp Val Asp Lys Gly Pro Gly Ser Thr
265           145          150          155          160
266 Lys Glu Leu Ile Lys Ser Ile Asn Glu Lys Phe Ala Gly Ser Ala Gly
267           165          170          175
268 Trp Glu Gly Thr Glu Ser Leu Lys Lys Pro Glu Asp Lys Lys Gln Leu
269           180          185          190
270 Gly Asp Phe Phe Gly Met Ser Asn Ser Tyr Ala Glu Cys Tyr Pro Ala
271           195          200          205
272 Thr Met Asp Asp Met Ala Val Asp Ser Asp Glu Glu Val Asp Tyr Ser
273           210          215          220
274 Lys Met Asp Gln Gly Asn Lys Lys Gly Pro Leu Gly Arg Trp Asp Phe
275           225          230          235          240
276 Asp Thr Gln Glu Glu Tyr Ser Glu Tyr Met Asn Asn Lys Glu Ala Leu
277           245          250          255
278 Pro Lys Ala Ala Phe Gln Tyr Gly Ile Lys Met Ser Glu Gly Arg Lys
279           260          265          270
280 Thr Arg Arg Phe Lys Glu Thr Asn Asp Lys Ala Glu Leu Asp Arg Gln
281           275          280          285
W--> 282 Trp Lys Lys Ile Ser Ala Ile Ile Xaa Glu Glu Glu Glu Asp Gly Ser
283           290          295          300

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285 <210> SEQ ID NO: 8

286 <211> LENGTH: 16

287 <212> TYPE: PRT

288 <213> ORGANISM: Homo sapiens

290 <400> SEQUENCE: 8

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291 Arg Arg Gln Thr Leu Ser His Gly Ser Ser Ser Pro Ala Arg Ala Cys
292   1           5           10           15

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/819,144

DATE: 06/13/2003
TIME: 08:30:04

Input Set : A:\21486-021DIV.txt
Output Set: N:\CRF4\06132003\I819144.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 14
Seq#:5; N Pos. 226,228,229,245,251,255,257,266,269,273,275,276,277,278,533
Seq#:5; N Pos. 534,546,548,553,617,619,627,630,633,647,653,655,661,669,671
Seq#:5; N Pos. 672,680,684,1732
Seq#:6; N Pos. 891
Seq#:6; Xaa Pos. 297
Seq#:7; Xaa Pos. 297

VERIFICATION SUMMARYPATENT APPLICATION: **US/09/819,144**

DATE: 06/13/2003

TIME: 08:30:04

Input Set : **A:\21486-021DIV.txt**Output Set: **N:\CRF4\06132003\I819144.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:180
M:341 Repeated in SeqNo=5
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:864
M:341 Repeated in SeqNo=6
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:288